What is claimed:

1. A method for isolating a labeled single stranded target polynucleotide comprising, forming a polymerase chain reaction (PCR) mixture comprising,

    a. a polynucleotide region of interest,

    b. a first primer specific for the region of interest, wherein the primer has a label and a mobility modifier,

    c. a second primer specific for the region of interest, wherein the second primer comprises an affinity moiety, thereby forming a reaction mixture,

amplifying the region of interest, thereby producing a double stranded polynucleotide amplification product comprising the labeled single stranded target polynucleotide comprising the label and the mobility modifier, and a complementary affinity moiety strand,

contacting the reaction mixture with a binding moiety specific for the affinity moiety,

binding the double stranded polynucleotide amplification product to the binding moiety,

removing the unbound unincorporated reaction components, and,

releasing the labeled single stranded target polynucleotide from the bound double stranded polynucleotide amplification product by denaturation.

2. The method according to claim 1 wherein said mobility modifier is chosen from the group comprising nucleotides, polyethylene oxide, polyglycolic acid, polylactic acid, polypeptide, oligosaccharide, and polyurethane, polyamide, polysulfonamide,

polysulfoxide, and block copolymers thereof, including polymers composed of units of multiple subunits linked by charged or uncharged linking groups, and combinations thereof.

3. The method according to claim 1 wherein the binding moiety is streptavidin.
4. The method according to claim 1 wherein the affinity moiety is biotin.
5. The method according to claim 1 wherein the PCR mixture further comprises a plurality of primer sets, each primer set comprising a first primer and a second primer flanking a region of interest, wherein the first primer further comprises the label and the mobility modifier, and wherein the second primer further comprises the affinity moiety
6. The method according to claim 5 wherein the polynucleotide region of interest is derived from a sample that further comprises degraded DNA.
7. The method according to claim 6 wherein said degraded DNA is between about 60 and 240 nucleotides in length.
8. The method according to claim 7 wherein the regions of interest further comprise polymorphic microsatellites.
9. The method according to claim 8 wherein the polymorphic microsatellites further comprise a dinucleotide repeat.
10. The method according to claim 8 wherein the polymorphic microsatellites further comprise a trinucleotide repeat.
11. The method according to claim 8 wherein the polymorphic microsatellites further comprise a tetranucleotide repeat.

12. The method according to claim 5 wherein at least one of the single stranded target polynucleotides results from amplification with a primer pair lacking a mobility modifier.

13. The method according to claim 1 wherein the PCR mixture further comprises sorbitol.

14. The method according to claim 1 wherein the PCR mixture further comprises betaine.

15. The method according to claim 1 wherein the PCR mixture further comprise sorbitol and betaine.

16. A method for manufacturing a labeled single stranded target polynucleotide molecular size standard comprising,

forming a PCR mixture comprising,

a. a polynucleotide region of interest,

b. a first primer specific for the region of interest, wherein the first primer comprises a label and a mobility modifier,

c. a second primer specific for the region of interest, wherein the second primer comprises an affinity moiety,

amplifying the region of interest, thereby producing a double stranded polynucleotide amplification product comprising the single stranded target polynucleotide molecular size standard comprising the label and the mobility modifier, and a complementary affinity moiety strand,

contacting the reaction mixture with a binding moiety specific for the affinity moiety,

binding the double stranded polynucleotide to the binding moiety,

removing the unbound unincorporated reaction components, and

releasing the labeled single stranded target polynucleotide molecular size standard.

17. The method according to claim 16 further comprising a plurality of regions of interest and a plurality of primer pairs, wherein a plurality of labeled single stranded target polynucleotide molecular size standards is formed.

18. A method for isolating a labeled single stranded target polynucleotide comprising,

forming a PCR mixture comprising,

a. a polynucleotide region of interest,

b. a first primer specific for the region of interest,

c. a second primer specific for the region of interest, wherein the second primer comprises an affinity moiety,

amplifying the region of interest, whereby a double stranded polynucleotide amplification product is produced, comprising an unlabelled single stranded target polynucleotide complement, and a complementary affinity moiety strand,

contacting the reaction mixture with a binding moiety specific for the affinity moiety,

binding the double stranded polynucleotide amplification product to the binding moiety,

removing the unbound unincorporated reaction components, and eluting and removing the unlabelled singled stranded target polynucleotide,

providing,

a. a polymerase,

b. a primer complementary to the bound second strand, wherein the primer further comprises a mobility modifier, and,

c. at least one dye-labelled nucleotide,

performing an extension reaction to form a labeled single stranded target polynucleotide, and,

releasing the labeled single stranded target polynucleotide.

19. The method according to claim 18 wherein the labeled single stranded polynucleotide is analyzed by a mobility-dependent analysis technique.

20. The method according to claim 19 wherein the mobility-dependent analysis technique is capillary electrophoresis.